The following listing of claims replaces all previous claims.

LISTING OF CLAIMS

1. (Canceled)

2. (Canceled)

3. (Currently amended) A method of analyzing micro-satellite loci, comprising steps of:

a) providing primers for co-amplifying a set of at least three microsatellite loci of human genomic DNA, comprising at least one mono-nucleotide repeat locus and at least two tetra-nucleotide repeat loci, wherein the at least one mononucleotide repeat locus comprises MONO-15 and wherein the at least two tetra-nucleotide repeat loci are selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51;

b) co-amplifying the set of at least three microsatellite loci from at least one sample of genomic DNA in a multiplex amplification reaction, using the primers, thereby producing amplified DNA fragments; and

c) determining the size of the amplified DNA fragments.

4. (Previously presented) A method of analyzing micro-satellite loci, comprising steps of:

a) providing primers for co-amplifying a set of at least three microsatellite loci of human genomic DNA, comprising at least one mono-nucleotide repeat locus and at least two tetra-nucleotide repeat loci, wherein the at least one mono-nucleotide repeat locus comprises MONO-15;

b) co-amplifying the set of at least three microsatellite loci from at least one sample of genomic DNA in a multiplex amplification reaction, using the primers, thereby producing amplified DNA fragments; and

c) determining the size of the amplified DNA fragments.

5. (Currently amended) The method of claim 4, wherein the set of at least three microsatellite loci is a set of at least five microsatellite loci, comprising:

at least two mono-nucleotide repeat loci comprising MONO-15 and at least one locus selected from the group consisting of BAT-25, BAT-26, and MONO-11, ~~and MONO-15~~; and

at least three tetra-nucleotide repeat loci selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

6. (Previously presented) The method of claim 4, wherein at least one of the primers provided in step (a) has a nucleic acid sequence selected from the group of primer sequences identified by: SEQ ID NO:7 and SEQ ID NO:8.

7. (Previously presented) The method of claim 4, wherein the set of at least three microsatellite loci is a set of at least nine microsatellite loci, comprising BAT-25, BAT-26, MONO-15, D1S518, D3S2432, D7S1808, D7S3070, D7S3046, D10S1426.

8. (Original) The method of claim 7, wherein the set of at least nine microsatellite loci is co-amplified using at least one primer for each locus selected from the group consisting of:

SEQ ID NO: 1 and SEQ ID NO: 60 when the locus is BAT-25,

SEQ ID NO: 61 and SEQ ID NO: 62 when the locus is BAT-26,

SEQ ID NO: 7 and SEQ ID NO: 8 when the locus is MONO-15,

SEQ ID NO: 49 and SEQ ID NO: 50 when the locus is D1S518,

SEQ ID NO: 17 and SEQ ID NO: 59 when the locus is D3S2432,

SEQ ID NO: 51 and SEQ ID NO: 52 when the locus is D7S1808,

SEQ ID NO: 53 and SEQ ID NO: 54 when the locus is D7S3070,

SEQ ID NO: 55 and SEQ ID NO: 56 when the locus is D7S3046, and

SEQ ID NO: 57 and SEQ ID NO: 58 when the locus is D10S1426.

9. (Previously presented) The method of claim 4, wherein the set of at least three microsatellite loci is co-amplified in step (c) using at least one oligonucleotide primer for each locus which is fluorescently labeled.

10. (Previously presented) The method of claim 4, wherein the at least one sample of genomic DNA comprises a first sample of genomic DNA originating from normal non-cancerous biological material from an individual and a second sample of genomic DNA originating from a tumor of the individual, the method further comprising:

detecting microsatellite instability by comparing the size of the amplified DNA fragments produced from co-amplifying the first sample of genomic DNA to the size of the amplified DNA fragments produced from co-amplifying the second sample of genomic DNA.

11. (Previously presented) The method of claim 10, further comprising correlating the microsatellite instability results with the prognosis.

12. (Previously presented) The method of claim 10, further comprising correlating the microsatellite instability results with familial tumor predisposition.

13. (Previously presented) The method of claim 10, further comprising correlating the microsatellite instability results with the presence of cancerous tumors of the gastro-intestinal system and of the endometrium.

14. (Original) The method of claim 13 wherein the cancerous tumors are tumors from a colorectal cancer.

15. (Canceled)

16. (Canceled)

17. (Previously presented) The method of claim 3, wherein the at least one sample of genomic DNA comprises a first sample of genomic DNA originating from normal non-cancerous biological material from an individual and a second sample of genomic DNA originating from a second biological material from the individual, and wherein the microsatellite loci of the first and second samples are co-amplified in separate multiplex amplification reactions, using the primers, thereby producing first amplified DNA fragments from the first sample and second amplified DNA fragments from the second sample; and further comprising:

d) comparing the size of first amplified DNA fragments to the size of the second amplified DNA fragments to detect instability in any of the microsatellite loci of the second genomic DNA.

18. (Previously presented) The method of claim 4, wherein the at least one sample of genomic DNA comprises a first sample of genomic DNA originating from normal non-cancerous biological material from an individual and a second sample of genomic DNA originating from a second biological material from the individual, and wherein the microsatellite loci of the first and second samples are co-amplified in separate multiplex amplification reactions, using the primers, thereby producing first amplified DNA fragments from the first sample and second amplified DNA fragments from the second sample; and further comprising:

d) comparing the size of first amplified DNA fragments to the size of the second amplified DNA fragments to detect instability in any of the microsatellite loci of the second genomic DNA.

19. (Currently amended) The method of claim 18, wherein the set of at least three microsatellite loci is a set of at least five microsatellite loci, comprising two mono-nucleotide repeat loci comprising MONO-15 and at least one mononucleotide repeat locus selected from the group consisting of BAT-25, BAT-26, and MONO-11~~, and MONO-15~~, and three tetra-nucleotide repeat loci selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

20. (Previously presented) The method of claim 18, wherein at least one of the primers provided in step (a) has a nucleic acid sequence selected from the group of primer sequences identified by: SEQ ID NO:7 and SEQ ID NO:8.

21. (Previously presented) The method of claim 18, wherein the at least one primer for each locus provided in step (a) is fluorescently labeled.

22. (Previously presented) The method of claim 18, wherein the set of at least three microsatellite loci is a set of at least nine microsatellite loci, comprising: BAT-25, BAT-26, MONO-15, D1S518, D3S2432, D7S1808, D7S3070, D7S3046, D10S1426.

23. (Original) The method of claim 22, wherein the set of at least nine microsatellite loci is co-amplified using at least one primer for each locus selected from the group consisting of:

SEQ ID NO: 1 and SEQ ID NO: 60 when the locus is BAT-25,

SEQ ID NO: 61 and SEQ ID NO: 62 when the locus is BAT-26,

SEQ ID NO: 7 and SEQ ID NO: 8 when the locus is MONO-15,

SEQ ID NO: 49 and SEQ ID NO: 50 when the locus is D1S518,

SEQ ID NO: 17 and SEQ ID NO: 59 when the locus is D3S2432,

SEQ ID NO: 51 and SEQ ID NO: 52 when the locus is D7S1808,

SEQ ID NO: 53 and SEQ ID NO: 54 when the locus is D7S3070,

SEQ ID NO: 55 and SEQ ID NO: 56 when the locus is D7S3046, and

SEQ ID NO: 57 and SEQ ID NO: 58 when the locus is D10S1426.

24. (Previously presented) The method of claim 18, wherein the second sample of biological material is selected from the group consisting of: tumor tissue, disseminated cells, feces, blood cells, blood plasma, serum, lymph nodes, urine, and other bodily fluids.

25. (Previously presented) The method of claim 18, wherein the microsatellite instability results are used in prognostic tumor diagnosis.

26. (Previously presented) The method of claim 18, wherein the microsatellite instability results are used in the diagnosis of familial tumor predisposition.

27. (Previously presented) The method of claim 18, wherein the microsatellite instability results are used to detect cancerous tumors of the gastro-intestinal system and of the endometrium.

28. (Original) The method of claim 27 wherein the cancerous tumors are tumors from a colorectal cancer.

29. (Previously presented) A method of analyzing at least one mono-nucleotide repeat locus, comprising the steps of:

a) providing at least one primer for at least one mono-nucleotide repeat locus of human genomic DNA, wherein the at least one mono-nucleotide repeat locus comprises MONO-15;

b) amplifying at least one mono-nucleotide repeat locus from a sample of genomic DNA originating from a biological material from an individual, using the at least one primer, thereby producing amplified DNA fragments; and

c) determining the size of the amplified DNA fragments.

30. (Previously presented) The method of claim 29, wherein the at least one mono-nucleotide repeat locus is co-amplified using at least one primer selected from the group consisting of: SEQ ID NO: and SEQ ID NO:8.

31. (Original) The method of claim 29, wherein the at least one mono-nucleotide repeat locus is amplified using at least one oligonucleotide primer which is fluorescently labeled.

32. (Original) The method of claim 29, wherein the biological material is selected from the group consisting of: tumor tissue, disseminated cells, feces, blood cells, blood plasma, serum, lymph nodes, urine, and other bodily fluids.

33. (Original) The method of claim 29, further comprising detecting microsatellite instability at the at least one mono-nucleotide repeat locus by comparing the size of the amplified DNA fragments to the most commonly observed allele size at that locus in a human population.

34. (Original) The method of claim 29, further comprising amplifying the at least one mono-nucleotide repeat locus of a sample of human genomic DNA from normal non-cancerous biological material from the individual, and comparing resulting second amplified DNA fragments to the amplified DNA fragments obtained in step (b) to detect microsatellite instability in step (c).

35-49. (Canceled)

50. Currently amended) A method of analyzing micro-satellite loci, comprising:

a) providing primers for co-amplifying a set of at least three microsatellite loci of human genomic DNA, ~~comprising at least one mono nucleotide repeat locus selected from the group consisting of BAT-25, BAT-26, MONO-11, and~~ comprising MONO-15 and at least two tetra-nucleotide repeat loci selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51;

b) co-amplifying the set of at least three microsatellite loci from at least one sample of genomic DNA in a multiplex amplification reaction, using the primers, thereby producing amplified DNA fragments; and

c) determining the size of the amplified DNA fragments.

51-55. (Canceled)